

WEST Search History

Hide Items

Restore

Clear

Cancel

DATE: Thursday, November 03, 2005

Hide?	Set Name	Query	Hit Count
	<i>DB=PGPB,USPT,EPAB; PLUR=YES; OP=OR</i>		
<input type="checkbox"/>	L51	L50 and l17	2
<input type="checkbox"/>	L50	(424/179.1)![CCLS]	249
<input type="checkbox"/>	L49	L48 and l17	1
<input type="checkbox"/>	L48	(530/387.1,387.3,388.1,388.8)![CCLS]	5526
<input type="checkbox"/>	L47	6022966.pn.	1
<input type="checkbox"/>	L46	L45 and L44	1
<input type="checkbox"/>	L45	cancer\$ or tumor\$ or neoplas\$	175849
<input type="checkbox"/>	L44	5541287.pn.	1
<input type="checkbox"/>	L43	L42 and L36	88
<input type="checkbox"/>	L42	L41 or L40 or L38	267
<input type="checkbox"/>	L41	L37.clm.	245
<input type="checkbox"/>	L40	L37.ti.	12
<input type="checkbox"/>	L39	L37.ti	3560
<input type="checkbox"/>	L38	L37.ab.	31
<input type="checkbox"/>	L37	dota	3560
<input type="checkbox"/>	L36	L34 or L35	2631
<input type="checkbox"/>	L35	(534/10)![CCLS]	751
<input type="checkbox"/>	L34	(424/1.11 424/1.49 424/1.53 424/1.65 424/1.69)![CCLS]	2091
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<input type="checkbox"/>	L32	5958374.pn.	1
<input type="checkbox"/>	L31	L30 or L29 or L27	3
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<input type="checkbox"/>	L29	5747654.pn.	1
<input type="checkbox"/>	L28	4722892	43
<input type="checkbox"/>	L27	4722892.pn.	1
<input type="checkbox"/>	L26	L25 with L2	3
<input type="checkbox"/>	L25	bifunctional adj antibod\$	1027
<input type="checkbox"/>	L24	L23 not @py>2002	27
<input type="checkbox"/>	L23	L21 and DOTA	57
<input type="checkbox"/>	L22	anti adj metal adj chelate adj antibod\$	13
<input type="checkbox"/>	L21	L20 with L2	551

<input type="checkbox"/>	L20	\$antibod\$	155175
<input type="checkbox"/>	L19	?antibod?	132
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<input type="checkbox"/>	L17	meares.in.	57
<input type="checkbox"/>	L16	L15 not @py>2002	74
<input type="checkbox"/>	L15	L13 and therap\$	288
<input type="checkbox"/>	L14	L13 not @py>2002	75
<input type="checkbox"/>	L13	L1 with L6	294
<input type="checkbox"/>	L12	L11 same L4	2
<input type="checkbox"/>	L11	TETA	4114
<input type="checkbox"/>	L10	L4 same L6	4
<input type="checkbox"/>	L9	L8 not @py>2002	23
<input type="checkbox"/>	L8	L4 and L6	41
<input type="checkbox"/>	L7	L6 and L5	29
<input type="checkbox"/>	L6	DOTA	3560
<input type="checkbox"/>	L5	L4 not @py>2003	254
<input type="checkbox"/>	L4	L1 with L2	375
<input type="checkbox"/>	L3	L2 and L1	4688
<input type="checkbox"/>	L2	metal adj chelat?	8427
<input type="checkbox"/>	L1	antibod?	126273

END OF SEARCH HISTORY

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OM protein - protein search, using sw model

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Run on:          October 28, 2005, 15:19:05 ; Search time 120 Seconds  
                (without alignments)  
                702.615 Million cell updates/sec
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Title: US-09-671-953B-5
Perfect score: 1132
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database :      A_Geneseq_16Dec04:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	8						
No.	Score	Query Match	Length	DB	ID		Description
1	1130	99.8	218	4	AAB20358		Aab20358 Anti-chel
2	1118	98.8	218	4	AAB20359		Aab20359 Anti-chel
3	1113	98.3	218	4	AAB20360		Aab20360 Anti-chel
4	1079	95.3	218	8	ADQ98050		Adq98050 Chimeric
5	1078	95.2	218	8	ADQ98051		Adq98051 Chimeric
6	776	68.6	215	8	ADR23362		Adr23362 Human CD7
7	759	67.0	235	2	AAW82740		Aaw82740 Plasmid p
8	755.5	66.7	235	5	AAE27925		Aae27925 Human C2B
9	755.5	66.7	235	6	ABB82834		Abb82834 Antibody

10	755	66.7	213	8	ADL92471	Adl92471	Antibody
11	751	66.3	220	2	AAW07528	Aaw07528	Anti-HGF
12	750.5	66.3	235	3	AAB08025	Aab08025	A dimeric
13	749.5	66.2	234	5	AAO14066	Aao14066	Light cha
14	749.5	66.2	234	6	ABU08018	Abu08018	Human mon
15	749.5	66.2	234	7	ADF65776	Adf65776	Human mon
16	749.5	66.2	234	8	ADJ92516	Adj92516	Human SOJ
17	749	66.2	213	6	AAE34878	Aae34878	BIWA4/8 a
18	749	66.2	213	8	ADL15445	Adl15445	Humanised
19	749	66.2	213	8	ADO00853	Ado00853	Humanised
20	747	66.0	213	6	AAE35326	Aae35326	Humanised
21	747	66.0	213	6	AAE34877	Aae34877	BIWA4 ant
22	747	66.0	213	8	ADL15441	Adl15441	Humanised
23	747	66.0	213	8	ADO00849	Ado00849	Humanised
24	746	65.9	215	8	ADQ31891	Adq31891	Antibody
25	746	65.9	239	8	ADK70470	Adk70470	Respirato
26	745.5	65.9	240	6	ABJ38595	Abj38595	Hepatitis
27	744	65.7	215	8	ADQ31885	Adq31885	Antibody
28	742	65.5	215	8	ADQ16702	Adq16702	Modified
29	742	65.5	236	8	ADP79579	Adp79579	Chimeric
30	741.5	65.5	234	3	AAV92239	Aay92239	Human bon
31	741	65.5	236	2	AAV34096	Aay34096	Partial a
32	740	65.4	213	4	AAB83157	Aab83157	Gangliosi
33	740	65.4	233	3	AAV93704	Aay93704	The kappa
34	740	65.4	233	3	AAV93731	Aay93731	The kappa
35	740	65.4	233	6	AAE35886	Aae35886	Human 4.8
36	739.5	65.3	214	2	AAV08599	Aay08599	Anti-huma
37	739	65.3	241	6	ABJ38593	Abj38593	Hepatitis
38	738.5	65.2	234	6	ABP55483	Abp55483	CJRA05 pr
39	738.5	65.2	240	6	ABJ38594	Abj38594	Hepatitis
40	738	65.2	235	2	AAW06180	Aaw06180	Humanised
41	737.5	65.2	214	8	ADH34591	Adh34591	023 light
42	737	65.1	213	2	AAW05830	Aaw05830	Humanised
43	737	65.1	215	6	ABR01469	Abr01469	Human ant
44	736.5	65.1	216	8	ADS87940	Ads87940	Anti-IFN-
45	736.5	65.1	216	8	ADS94937	Ads94937	Anti-IFN-

ALIGNMENTS

RESULT 1

AAB20358

ID AAB20358 standard; protein; 218 AA.

XX

AC AAB20358;

XX

DT 11-JUN-2001 (first entry)

XX

DE Anti-chelate antibody CHA255 light chain mutant N96C.

XX

KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;

KW cancer; therapy; mutant; mutein.

XX

OS Mus musculus.

OS Synthetic.

XX

FH	Key	Location/Qualifiers
FT	Region	1. .23
FT		/label= FR1
FT		/note= "framework region 1"
FT	Region	24. .37
FT		/label= CDR1
FT		/note= "complementarity determining region 1"
FT	Region	38. .52
FT		/label= FR2
FT		/note= "framework region 2"
FT	Region	53. .59
FT		/label= CDR2
FT		/note= "complementarity determining region 2"
FT	Region	60. .92
FT		/label= FR3
FT		/note= "framework region 3"
FT	Region	93. .100
FT		/label= CDR3
FT		/note= "complementarity determining region 3"
FT	Misc-difference	96
FT		/note= "replaces Asn of wild-type sequence"
FT	Misc-difference	100
FT		/note= "encoded by GTR"
FT	Region	101. .131
FT		/label= FR4
FT		/note= "framework region 4"
FT	Misc-difference	112
FT		/note= "encoded by CGW"
FT	Misc-difference	113
FT		/note= "encoded by ACK"
FT	Misc-difference	206
FT		/note= "encoded by AGY"
FT	Misc-difference	207
FT		/note= "encoded by TYG"
XX		
PN	WO200122922-A2.	
XX		
PD	05-APR-2001.	
XX		
PF	27-SEP-2000; 2000WO-US026619.	
XX		
PR	27-SEP-1999; 99US-0156194P.	
PR	31-MAY-2000; 2000US-0208684P.	
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Meares C, Chmura A;	
XX		
DR	WPI; 2001-244971/25.	
DR	N-PSDB; AAF30633.	
XX		
PT	Nucleic acid encoding a mutant antibody comprising a reactive site that	
PT	specifically binds to a metal chelate useful as analytical agents and in	
PT	clinical diagnosis, as well as in the treatment of disease, particularly	
PT	cancer.	
XX		
PS	Disclosure; Fig 12; 100pp; English.	

XX
 CC The invention provides a mutant antibody comprising a reactive site that
 CC is not present in the wild-type of the antibody. The antibody also has a
 CC complementarity determining region (CDR) that specifically binds to a
 CC metal chelate against which the wild-type antibody is raised. The
 CC reactive site of the mutant antibody is in a position proximate to or
 CC within the CDR, such that the chelate and the antibody are able to form a
 CC covalent bond. The present sequence is that of the light chain variable
 CC region of anti-indium-EDTA monoclonal antibody CHA255, carrying an N96C
 CC mutation. As an example of the method of the invention, rational computer
 CC -aided design was used to develop an indium-EDTA chelate to covalently
 CC bind to CHA255 in vivo. The premise was to allow the chelate to bind non-
 CC covalently to CHA255 bound to a tumour and then to covalently attach the
 CC chelate to the antibody, thereby trapping it at the tumour site. This
 CC involved cloning the variable domains of CHA255 to construct a
 CC human/mouse chimeric Fab fragment that could be expressed in Escherichia
 CC coli, and the synthesis and screening of benzyl-EDTA chelates carrying
 CC weakly electrophilic groups capable of conjugation of the antibody in
 CC vivo. This Fab can be conjugated to a targeting moiety when desired. A
 CC reactive site was incorporated into the antibody by engineering a Cys
 CC residue at location Asn-96 or Ser-95 of the light chain, near the region
 CC of the antibody to which the chelate bound. This was accomplished by site
 CC -directed mutagenesis of a nucleic acid encoding the wild-type of the
 CC anti-chelate antibody
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 SQ Sequence 218 AA;

Query Match 99.8%; Score 1130; DB 4; Length 218;
 Best Local Similarity 100.0%; Pred. No. 7.4e-80;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSAVVTQESALTTSPGETVTTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
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 Db 1 RSAVVTQESALTTSPGETVTTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
 Qy 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
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 Db 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
 Qy 121 IFPPSDEQLKSGTASVCLNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
 |||
 Db 121 IFPPSDEQLKSGTASVCLNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
 Qy 181 STLTLKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
 |||
 Db 181 STLTLKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218

RESULT 2

AAB20359

ID AAB20359 standard; protein; 218 AA.
 XX
 AC AAB20359;
 XX
 DT 11-JUN-2001 (first entry)
 XX
 DE Anti-chelate antibody CHA255 light chain.

XX
 KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;
 KW cancer; therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 1. .23
 FT /label= FR1
 FT /note= "framework region 1"
 FT Region 24. .37
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 38. .52
 FT /label= FR2
 FT /note= "framework region 2"
 FT Region 53. .59
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 60. .92
 FT /label= FR3
 FT /note= "framework region 3"
 FT Region 93. .100
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
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 FT Region 101. .131
 FT /label= FR4
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 FT Misc-difference 112
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 FT Misc-difference 113
 FT /note= "encoded by ACK"
 FT Misc-difference 206
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 FT Misc-difference 207
 FT /note= "encoded by TYG"
 XX
 PN WO200122922-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 27-SEP-2000; 2000WO-US026619.
 XX
 PR 27-SEP-1999; 99US-0156194P.
 PR 31-MAY-2000; 2000US-0208684P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Meares C, Chmura A;
 XX
 DR WPI; 2001-244971/25.
 DR N-PSDB; AAF30634.
 XX
 PT Nucleic acid encoding a mutant antibody comprising a reactive site that
 PT specifically binds to a metal chelate useful as analytical agents and in

DT 11-JUN-2001 (first entry)
 XX
 DE Anti-chelate antibody CHA255 light chain mutant S95C.
 XX
 KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;
 KW cancer; therapy; mutant; mutein.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1. .23
 FT /label= FR1
 FT /note= "framework region 1"
 FT Region 24. .37
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 38. .52
 FT /label= FR2
 FT /note= "framework region 2"
 FT Region 53. .59
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 60. .92
 FT /label= FR3
 FT /note= "framework region 3"
 FT Region 93. .100
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FT Misc-difference 95
 FT /note= "replaces Ser of wild-type sequence"
 FT Misc-difference 100
 FT /note= "encoded by GTR"
 FT Region 101. .131
 FT /label= FR4
 FT /note= "framework region 4"
 FT Misc-difference 112
 FT /note= "encoded by CGW"
 FT Misc-difference 113
 FT /note= "encoded by ACK"
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 FT /note= "encoded by AGY"
 FT Misc-difference 207
 FT /note= "encoded by TYG"
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 PN WO200122922-A2.
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 PD 05-APR-2001.
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 PF 27-SEP-2000; 2000WO-US026619.
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 PR 27-SEP-1999; 99US-0156194P.
 PR 31-MAY-2000; 2000US-0208684P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Meares C, Chmura A;

XX
DR WPI; 2001-244971/25.
DR N-PSDB; AAF30635.
XX
PT Nucleic acid encoding a mutant antibody comprising a reactive site that
PT specifically binds to a metal chelate useful as analytical agents and in
PT clinical diagnosis, as well as in the treatment of disease, particularly
PT cancer.
XX
PS Disclosure; Fig 14; 100pp; English.
XX
CC The invention provides a mutant antibody comprising a reactive site that
CC is not present in the wild-type of the antibody. The antibody also has a
CC complementarity determining region (CDR) that specifically binds to a
CC metal chelate against which the wild-type antibody is raised. The
CC reactive site of the mutant antibody is in a position proximate to or
CC within the CDR, such that the chelate and the antibody are able to form a
CC covalent bond. The present sequence is that of the light chain variable
CC region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C
CC mutation. As an example of the method of the invention, rational computer
CC -aided design was used to develop an indium-EDTA chelate to covalently
CC bind to CHA255 in vivo. The premise was to allow the chelate to bind non-
CC covalently to CHA255 bound to a tumour and then to covalently attach the
CC chelate to the antibody, thereby trapping it at the tumour site. This
CC involved cloning the variable domains of CHA255 to construct a
CC human/mouse chimeric Fab fragment that could be expressed in Escherichia
CC coli, and the synthesis and screening of benzyl-EDTA chelates carrying
CC weakly electrophilic groups capable of conjugation of the antibody in
CC vivo. This Fab can be conjugated to a targeting moiety when desired. A
CC reactive site was incorporated into the antibody by engineering a Cys
CC residue at location Asn-96 or Ser-95 of the light chain, near the region
CC of the antibody to which the chelate bound. This was accomplished by site
CC -directed mutagenesis of a nucleic acid encoding the wild-type of the
CC anti-chelate antibody
XX
SQ Sequence 218 AA;

Query Match 98.3%; Score 1113; DB 4; Length 218;
Best Local Similarity 99.1%; Pred. No. 1.6e-78;
Matches 216; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db	1	RS	AVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG	60
Qy	61	VP	ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF	120
Db	61	VP	ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF	120
Qy	121	IF	PPSDEQLKSGTASVVCLLNNFYPPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	180
Db	121	IF	PPSDEQLKSGTASVVCLLNNFYPPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	180
Qy	181	ST	LTLKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC	218
Db	181	ST	LTLKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC	218

RESULT 4

ADQ98050

ID ADQ98050 standard; protein; 218 AA.

XX

AC ADQ98050;

XX

DT 21-OCT-2004 (first entry)

XX

DE Chimeric murine 2D12.5 variable light chain fused to human TTCL protein.

XX

KW murine; mouse; chimeric; human; TTCL; tetanus toxin;

KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;

KW single photon emission tomography; SPET; cancer; cytostatic;

KW immunosuppressive; multi-functional antibody; metal chelate;

KW antigen recognition domain; in vivo imaging;

KW cell-antibody-metal chelate complex; emission tomography.

XX

OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

XX

PN WO2004065569-A2.

XX

PD 05-AUG-2004.

XX

PF 23-JAN-2004; 2004WO-US001808.

XX

PR 23-JAN-2003; 2003US-00350555.

PR 22-JUL-2003; 2003US-00625047.

PR 31-JUL-2003; 2003US-00631258.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Meares C, Corneillie T;

XX

DR WPI; 2004-580725/56.

DR N-PSDB; ADQ98054.

XX

PT Novel mutant antibody comprising reactive site not present in wild-type

PT of antibody and antigen recognition domain that recognizes macrocyclic

PT metal chelate having four nitrogen atoms, useful for treating cancer or

PT autoimmune diseases.

XX

PS Claim 41; SEQ ID NO 27; 208pp; English.

XX

CC This invention relates to multi-functional antibodies that recognise

CC chelating agents and metal chelates, particularly macrocyclic metal

CC chelates. Specifically, it refers to an antibody that comprises a metal

CC chelate bound to an antigen recognition domain, where the metal chelate

CC has a reactive functional group of complementary reactivity to the

CC reactive site of the antibody. This reactive site is the side chain of a

CC naturally occurring amino acid e.g. the -SH group side chain of a

CC cysteine residue (not present in the wild type) which can be used to form

CC a covalent bond between the reactive site of the antibody and the

CC reactive functional group of the metal chelate. The present invention

CC describes using these antibodies for in vivo imaging where the antibody

FH Key Location/Qualifiers
 FT Misc-difference 55
 FT /note= "Wild type Asn substituted for Cys"
 XX
 PN WO2004065569-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 23-JAN-2004; 2004WO-US001808.
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 PR 23-JAN-2003; 2003US-00350555.
 PR 22-JUL-2003; 2003US-00625047.
 PR 31-JUL-2003; 2003US-00631258.
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 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Meares C, Corneillie T;
 XX
 DR WPI; 2004-580725/56.
 DR N-PSDB; ADQ98055.
 XX
 PT Novel mutant antibody comprising reactive site not present in wild-type
 PT of antibody and antigen recognition domain that recognizes macrocyclic
 PT metal chelate having four nitrogen atoms, useful for treating cancer or
 PT autoimmune diseases.
 XX
 PS Claim 41; SEQ ID NO 28; 208pp; English.
 XX
 CC This invention relates to multi-functional antibodies that recognise
 CC chelating agents and metal chelates, particularly macrocyclic metal
 CC chelates. Specifically, it refers to an antibody that comprises a metal
 CC chelate bound to an antigen recognition domain, where the metal chelate
 CC has a reactive functional group of complementary reactivity to the
 CC reactive site of the antibody. This reactive site is the side chain of a
 CC naturally occurring amino acid e.g. the -SH group side chain of a
 CC cysteine residue (not present in the wild type) which can be used to form
 CC a covalent bond between the reactive site of the antibody and the
 CC reactive functional group of the metal chelate. The present invention
 CC describes using these antibodies for in vivo imaging where the antibody
 CC comprises a targeting moiety that binds specifically to a cell via a cell
 CC surface receptor or antigen thus forming a cell-mutant antibody complex.
 CC On addition of the metal chelate, a cell-antibody-metal chelate complex
 CC is formed that can be detected using emission tomography, magnetic
 CC resonance imaging, lanthanide luminescence, gamma-emissions or single
 CC photon emission tomography (SPET). As such, this method is useful for
 CC treating a subject with cancer and pharmaceutical compositions exhibit
 CC cytostatic and immunosuppressive activities. This polypeptide sequence is
 CC the chimeric mutant N53C murine antibody 2D12.5 variable light chain
 CC protein fused to the human anti-tetanus toxin antibody kappa light chain
 CC constant region of the invention.
 XX
 SQ Sequence 218 AA;

Query Match 95.2%; Score 1078; DB 8; Length 218;
 Best Local Similarity 95.9%; Pred. No. 8.2e-76;
 Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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 Db 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGCNNRPPG 60

Qy 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
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 Db 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120

Qy 121 IFPPSDEQLKSGTASVCLNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
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Qy 181 STLTLKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
 |||
 Db 181 STLTLKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218

RESULT 6

ADR23362

ID ADR23362 standard; protein; 215 AA.

XX

AC ADR23362;

XX

DT 04-NOV-2004 (first entry)

XX

DE Human CD72-targeted IgG1 light chain.

XX

KW Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;
 KW immunosuppressive; cancer; autoimmune disease; gene therapy.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
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FT	Region	1. .109
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FT		/label= V_region
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FT	Region	110. .215
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XX

PN WO2004067569-A1.

XX

PD 12-AUG-2004.

XX

PF 27-JAN-2003; 2003WO-EP050004.

XX

PR 27-JAN-2003; 2003WO-EP050004.

XX

PA (CRUC-) CRUCCELL HOLLAND BV.

XX

PI Bakker ABH, Marissen WE;

XX

DR WPI; 2004-580978/56.

DR N-PSDB; ADR23361.

XX

PT New internalizing human binding molecules capable of specifically binding
 PT to CD72, useful for diagnosing and/or treating B-cell associated
 PT diseases, such as cancer or autoimmune disorders.

XX

PS Example 5; SEQ ID NO 54; 174pp; English.

XX

CC The present sequence is the protein sequence of the light chain of human
CC IgG1 antibody 025, which specifically recognises human B cell associated
CC antigen CD72. An scFv ADR23324 selected from an antibody phage display
CC library was shown to specifically recognise the human CD72 receptor. The
CC scFv was recloned in IgG expression vector C01 using primers designed to
CC restore complete human frameworks, thereby generating antibody 025. Such
CC anti-CD72 immunoglobulins or their antigen-binding fragments can be used
CC as internalising human binding molecules of the invention. These
CC internalising human binding molecules are capable of (specifically)
CC binding to CD72 or its antigenic determinant, and preferably bind to CD72
CC associated with cells. Upon binding to CD72 present on the surface of
CC target cells, the binding molecules internalise. In addition to the
CC internalising human binding molecules, the invention provides
CC immunoconjugates comprising an internalising human binding molecule and a
CC tag (toxic substance, radioactive substance, liposome and/or enzyme),
CC nucleic acids encoding these, and compositions comprising them. The
CC internalising human binding molecule, immunoconjugate, nucleic acid
CC molecule or composition can be used in the diagnosis and/or treatment of
CC a B cell associated disorder or disease, especially a B cell associated
CC cancer and B cell associated autoimmune disorder (claimed).

XX

SQ Sequence 215 AA;

Query Match 68.6%; Score 776; DB 8; Length 215;
Best Local Similarity 73.5%; Pred. No. 2.4e-52;
Matches 161; Conservative 16; Mismatches 36; Indels 6; Gaps 3;

Qy 2 SAVVTQESALTTSPGETVTLTCSRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV 61
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Db 1 SSELTDQDPAVSVALGQTVRITCQ---GDSLRSYYASWYQQKPGQAPVPLVIYGKNNRPSGI 57

Qy 62 PARFSGSLIGDKAALTITGAQTEDEARYFCALWYSC--LWVFGGGTKLTVLSRTVAAPSV 119
| |||| |: |:||||| ||| |:| | ||||| |||||
Db 58 PDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLG-TVAAPSV 116

Qy 120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
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Db 117 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176

Qy 180 SSTLTLSKADYEEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Db 177 SSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC 215

us-09-671-953b-5.ra1

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2005, 15:23:21 ; Search time 30 Seconds
(without alignments)
542.450 Million cell updates/sec

Title: US-09-671-953B-5
Perfect score: 1132
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	759	67.0	235	3	US-09-423-439-18	Sequence 18, Appl
2	751	66.3	220	3	US-08-952-235-1	Sequence 1, Appli
3	751	66.3	220	4	US-09-669-971-1	Sequence 1, Appli
4	740	65.4	233	4	US-09-472-087-15	Sequence 15, Appl
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6	738	65.2	235	4	US-09-011-769A-27	Sequence 27, Appl
7	735	64.9	213	3	US-08-397-411-12	Sequence 12, Appl
8	734.5	64.9	491	4	US-10-011-125A-2	Sequence 2, Appli
9	734	64.8	236	4	US-09-315-926A-79	Sequence 79, Appl
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12	730.5	64.5	214	4	US-09-472-087-71	Sequence 71, Appl
13	730.5	64.5	224	4	US-09-456-090A-84	Sequence 84, Appl
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15	729.5	64.4	234	4	US-09-472-087-17	Sequence 17, Appl
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36	723	63.9	219	4	US-09-234-340A-72	Sequence 72, Appl
37	723	63.9	239	4	US-09-627-896B-22	Sequence 22, Appl
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45	722	63.8	214	3	US-08-437-642B-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-09-423-439-18

; Sequence 18, Application US/09423439
; Patent No. 6339070

GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles

BLAKEY, David Charles

TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L.L.P.

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423,439

FILING DATE: 09-No. 6339070-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294

FILING DATE: 05-MAY-1998

APPLICATION NUMBER: GB 9709421.3

FILING DATE: 10-MAY-1997

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us-09-671-953b-5.ra
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: SEQUENCE CHARACTERISTICS:
:   LENGTH: 235 amino acids
:   TYPE: amino acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:   MOLECULE TYPE: protein
:   SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-423-439-18

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Query Match          67.0%;  Score 759;  DB 3;  Length 235;
Best Local Similarity 72.2%;  Pred. No. 1.6e-67;
Matches 156;  Conservative 15;  Mismatches 39;  Indels 6;  Gaps 3;

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us-09-671-953b-5.rapb

GenCore version 5.1.6
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Run on: October 28, 2005, 15:34:17 ; Search time 113.5 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1078	95.2	218	16 US-10-625-047-28	Sequence 28, Appl
5	1078	95.2	218	17 US-10-631-258-28	Sequence 28, Appl
6	1078	95.2	218	18 US-10-350-555-28	Sequence 28, Appl
7	755.5	66.7	235	16 US-10-723-003-42	Sequence 42, Appl
8	755.5	66.7	235	20 US-11-004-639-42	Sequence 42, Appl
9	755	66.7	213	17 US-10-822-231-3	Sequence 3, Appli
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11	755	66.7	213	18 US-10-880-320-49	Sequence 49, Appl
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ALIGNMENTS

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 ; Publication No. US20040198962A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meares, Claude
 ; APPLICANT: Corneillie, Todd
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Multi-Functional Antibodies
 ; FILE REFERENCE: 023070-130910US
 ; CURRENT APPLICATION NUMBER: US/10/625,047
 ; CURRENT FILING DATE: 2003-07-22
 ; PRIOR APPLICATION NUMBER: US 10/350,555
 ; PRIOR FILING DATE: 2003-01-23

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; NUMBER OF SEQ ID NOS: 72
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:native cloned
;   OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region
;   OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody
;   OTHER INFORMATION: kappa light chain constant region (TTCL)
US-10-625-047-27

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GenCore version 5.1.6
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Maximum Match 100%
Listing first 45 summaries

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4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	716	63.3	215	2	JE0243		Ig kappa chain NIG
5	682.5	60.3	216	2	JE0241		Ig kappa chain Am3
6	675	59.6	215	2	A23746		Ig kappa chain V-I
7	578.5	51.1	135	2	S52059		JC-kappa protein -
8	552.5	48.8	240	2	S06084		Ig kappa chain pre
9	544	48.1	106	1	K3HU		Ig kappa chain C r
10	543.5	48.0	287	4	PC4402		pelB leader/Ig hea
11	537	47.4	128	2	S52450		Ig lambda chain V
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19	514	45.4	225	2	S37484	Ig kappa chain - m
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22	509	45.0	99	2	A37927	Ig kappa chain C r
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24	503.5	44.5	218	2	S68241	Ig kappa chain V r
25	503	44.4	99	2	S26653	Ig kappa chain C r
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32	492	43.5	217	2	S42772	Ig kappa chain - m
33	492	43.5	219	2	S16112	Ig kappa chain V r
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36	485	42.8	235	2	S25749	Ig lambda chain -
37	484.5	42.8	99	2	PH1089	Ig lambda chain V
38	482	42.6	99	2	S14582	Ig lambda chain V
39	482	42.6	113	2	S06821	Ig lambda chain V
40	482	42.6	219	2	S52028	Ig kappa chain - m
41	477	42.1	97	2	PH1090	Ig lambda chain V
42	477	42.1	116	1	L1MSV	Ig lambda-1 chain
43	475.5	42.0	210	2	A56169	Ig kappa chain V r
44	472	41.7	99	2	S14584	Ig lambda chain V
45	469	41.4	100	2	PH1088	Ig lambda chain V

ALIGNMENTS

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C;Species: Homo sapiens (man)

C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C;Accession: JE0242

R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.

submitted to JIPID, November 1998

A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Multiple deletions found in a VkIV protein.

A;Reference number: JE0241

A;Accession: JE0242

A;Molecule type: protein

A;Residues: 1-215 <ALI>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 740; DB 2; Length 215;
Best Local Similarity 70.4%; Pred. No. 7.9e-49;

Matches 152; Conservative 17; Mismatches 43; Indels 4; Gaps 3;

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Qy      4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62
      |:||  |: ||||  ||:|:|  ::||  | |:||  : ||  ::|| |:|
Db      3 VLTQSPGTLSSLSPGERATLSCRAS--QSVSNYYLAWYQQKPGQAPSLLIYDASSRATGIP 60

Qy     63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
      ||||  |  ||:| : || | |:| :  | || |||: : |||||
Db     61 DRFSGSGSGTDFILTISGLEPEDFAVYYCQQYDRPPWTFGQGTKVEI-KRTVAAPSVFIF 119

Qy    123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSS 182
      |||||
Db    120 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSS 179

Qy    183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
      |||||
Db    180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
```


us-09-671-953b-5.rup

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2005, 15:22:03 ; Search time 116.5 Seconds
(without alignments)
958.225 Million cell updates/sec

Title: US-09-671-953B-5
Perfect score: 1132
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	734	64.8	235	2	Q6PJF2	Q6pjf2 homo sapien
2	733	64.8	235	2	Q6GMW0	Q6gmw0 homo sapien
3	732	64.7	236	2	Q6GMW1	Q6gmw1 homo sapien
4	727.5	64.3	236	2	Q7Z3Y4	Q7z3y4 homo sapien
5	727	64.2	234	2	Q7Z473	Q7z473 homo sapien
6	723.5	63.9	236	2	Q6PIH7	Q6pih7 homo sapien
7	722.5	63.8	236	2	Q6GMX9	Q6gmx9 homo sapien
8	721.5	63.7	236	2	Q6P5S8	Q6p5s8 homo sapien
9	721	63.7	235	2	Q6GMV9	Q6gmv9 homo sapien
10	720.5	63.6	236	2	Q6GMX0	Q6gmx0 homo sapien
11	717.5	63.4	236	2	Q6PIL8	Q6pil8 homo sapien
12	715.5	63.2	236	2	Q6GMX8	Q6gmx8 homo sapien
13	704	62.2	236	2	Q6PIT5	Q6pit5 homo sapien
14	702.5	62.1	236	2	Q6PIH4	Q6pih4 homo sapien
15	697	61.6	239	2	Q8TCD0	Q8tcd0 homo sapien
16	696	61.5	240	2	Q6PIH6	Q6pih6 homo sapien
17	694	61.3	239	2	Q8NEK0	Q8nek0 homo sapien
18	666	58.8	239	2	Q6P491	Q6p491 homo sapien
19	564.5	49.9	120	2	Q6P5R5	Q6p5r5 homo sapien
20	544	48.1	106	1	KAC_HUMAN	P01834 homo sapien
21	535	47.3	129	1	LV1E_MOUSE	P01727 mus musculu

					us-09-671-953b-5.rup	
22	530	46.8	129	1	LV1D_MOUSE	P01726 mus musculu
23	529	46.7	129	1	LV1B_MOUSE	P01724 mus musculu
24	523	46.2	129	2	Q8VDE2	Q8vde2 mus musculu
25	522.5	46.2	238	2	Q66JS7	Q66js7 mus musculu
26	521	46.0	110	1	LV1C_MOUSE	P01725 mus musculu
27	514.5	45.5	113	2	Q8CGS1	Q8cgs1 mus musculu
28	510.5	45.1	236	2	Q7TS98	Q7ts98 mus musculu
29	507.5	44.8	109	2	Q9ET13	Q9et13 mus musculu
30	502	44.3	219	2	Q65ZC0	Q65zc0 mus musculu
31	497.5	43.9	241	2	Q63ZX4	Q63zx4 mus musculu
32	491	43.4	129	1	LV2B_MOUSE	P01729 mus musculu
33	477	42.1	117	1	LV1A_MOUSE	P01723 mus musculu
34	454	40.1	117	1	LV2A_MOUSE	P01728 mus musculu
35	442.5	39.1	236	2	Q8NEJ1	Q8nej1 homo sapien
36	440	38.9	235	2	Q6IN99	Q6in99 homo sapien
37	435	38.4	248	2	Q7SYU1	Q7syu1 xenopus lae
38	432	38.2	233	2	Q8TBC9	Q8tbc9 homo sapien
39	430.5	38.0	230	2	Q7Z2U3	Q7z2u3 homo sapien
40	430.5	38.0	236	2	Q6PIQ7	Q6piq7 homo sapien
41	428.5	37.9	236	2	Q6GMV7	Q6gmv7 homo sapien
42	428.5	37.9	236	2	Q6IPQ0	Q6ipq0 homo sapien
43	427.5	37.8	234	2	Q7Z2U7	Q7z2u7 homo sapien
44	426.5	37.7	236	2	Q6GMX4	Q6gmx4 homo sapien
45	426	37.6	231	2	Q6GNB8	Q6gnb8 xenopus lae

ALIGNMENTS

RESULT 1

Q6PJF2

ID Q6PJF2 PRELIMINARY; PRT; 235 AA.
AC Q6PJF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

us-09-671-953b-5.rup

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA Strausberg R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC016380; AAH16380.1; -.

DR HSSP; P01837; 1KCU.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; C1-set; 1.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGc1; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 64.8%; Score 734; DB 2; Length 235;
 Best Local Similarity 70.4%; Pred. No. 1.5e-56;
 Matches 152; Conservative 18; Mismatches 42; Indels 4; Gaps 3;

Qy	4	VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP	62
		:: :: :: :: : : :: :: ::: ::	
Db	23	VLTQSPATLSLSPGERATLSCRAS--QIVSSAYLAWYQQKPGQAPRLLMFGSSSRATGIP	80
Qy	63	ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF	122
		:: : :: : :: : :: :	
Db	81	DRFSGSGSGTDFTLTISRLEPEDFAVYCYQQYGSSQGTFGPGTKVDI-KRTVAAPSVFIF	139
Qy	123	PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSST	182
Db	140	PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSST	199
Qy	183	LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC	218
Db	200	LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	235

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OM protein - protein search, using sw model

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Run on:      October 28, 2005, 15:19:05 ; Search time 120 Seconds  
            (without alignments)  
            702.615 Million cell updates/sec
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Title: US-09-671-953B-7
Perfect score: 1134
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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1:  geneseqp1980s:*
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3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8							
Result	Query			DB			
No.	Score	Match	Length	ID	Description		
1	1132	99.8	218	4	AAB20360	Aab20360	Anti-chel
2	1122	98.9	218	4	AAB20359	Aab20359	Anti-chel
3	1113	98.1	218	4	AAB20358	Aab20358	Anti-chel
4	1083	95.5	218	8	ADQ98050	Adq98050	Chimeric
5	1082	95.4	218	8	ADQ98051	Adq98051	Chimeric
6	779	68.7	215	8	ADR23362	Adr23362	Human CD7
7	759.5	67.0	235	5	AAE27925	Aae27925	Human C2B
8	759.5	67.0	235	6	ABB82834	Abb82834	Antibody
9	759	66.9	213	8	ADL92471	Adl92471	Antibody

10	757	66.8	235	2	AAW82740	Aaw82740	Plasmid p
11	754.5	66.5	235	3	AAB08025	Aab08025	A dimeric
12	753	66.4	213	6	AAE34878	Aae34878	BIWA4/8 a
13	753	66.4	213	8	ADL15445	Adl15445	Humanised
14	753	66.4	213	8	ADO00853	Ado00853	Humanised
15	751	66.2	213	6	AAE35326	Aae35326	Humanised
16	751	66.2	213	6	AAE34877	Aae34877	BIWA4 ant
17	751	66.2	213	8	ADL15441	Adl15441	Humanised
18	751	66.2	213	8	ADO00849	Ado00849	Humanised
19	751	66.2	236	8	ADP79579	Adp79579	Chimeric
20	750	66.1	220	2	AAW07528	Aaw07528	Anti-HGF
21	746	65.8	215	8	ADQ31891	Adq31891	Antibody
22	744	65.6	215	8	ADQ31885	Adq31885	Antibody
23	743.5	65.6	234	5	AAO14066	Aao14066	Light cha
24	743.5	65.6	234	6	ABU08018	Abu08018	Human mon
25	743.5	65.6	234	7	ADF65776	Adf65776	Human mon
26	743.5	65.6	234	8	ADJ92516	Adj92516	Human SOJ
27	743	65.5	233	3	AA93704	Aay93704	The kappa
28	743	65.5	233	3	AA93731	Aay93731	The kappa
29	743	65.5	233	6	AAE35886	Aae35886	Human 4.8
30	743	65.5	239	8	ADK70470	Adk70470	Respirato
31	741.5	65.4	240	6	ABJ38595	Abj38595	Hepatitis
32	741	65.3	213	2	AAW05830	Aaw05830	Humanised
33	740.5	65.3	234	3	AA92239	Aay92239	Human bon
34	739.5	65.2	234	6	ABP55483	Abp55483	CJRA05 pr
35	739	65.2	215	8	ADQ16702	Adq16702	Modified
36	738	65.1	213	6	AAE33521	Aae33521	Human AQC
37	738	65.1	232	8	ADP79583	Adp79583	2H7.v16 L
38	736	64.9	235	2	AAW06180	Aaw06180	Humanised
39	736	64.9	236	2	AA934096	Aay34096	Partial a
40	735.5	64.9	214	8	ADH34591	Adh34591	023 light
41	735.5	64.9	349	2	AAR12128	Aar12128	1B1 IgG a
42	735.5	64.9	414	2	AAR13111	Aar13111	1B1 IgG a
43	735.5	64.9	414	2	AAR13018	Aar13018	1B1 IgG a
44	735	64.8	213	4	AAB83157	Aab83157	Gangliosi
45	735	64.8	215	6	ABR01469	Abr01469	Human ant

ALIGNMENTS

RESULT 1

AAB20360

ID AAB20360 standard; protein; 218 AA.

XX

AC AAB20360;

XX

DT 11-JUN-2001 (first entry)

XX

DE Anti-chelate antibody CHA255 light chain mutant S95C.

XX

KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;

KW cancer; therapy; mutant; mutein.

XX

OS Mus musculus.

OS Synthetic.

XX

FH	Key	Location/Qualifiers
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FT	Region	24. .37
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FT		/note= "complementarity determining region 1"
FT	Region	38. .52
FT		/label= FR2
FT		/note= "framework region 2"
FT	Region	53. .59
FT		/label= CDR2
FT		/note= "complementarity determining region 2"
FT	Region	60. .92
FT		/label= FR3
FT		/note= "framework region 3"
FT	Region	93. .100
FT		/label= CDR3
FT		/note= "complementarity determining region 3"
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FT	Misc-difference	100
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FT	Region	101. .131
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FT		/note= "encoded by CGW"
FT	Misc-difference	113
FT		/note= "encoded by ACK"
FT	Misc-difference	206
FT		/note= "encoded by AGY"
FT	Misc-difference	207
FT		/note= "encoded by TYG"
XX		
PN		WO200122922-A2.
XX		
PD		05-APR-2001.
XX		
PF		27-SEP-2000; 2000WO-US026619.
XX		
PR		27-SEP-1999; 99US-0156194P.
PR		31-MAY-2000; 2000US-0208684P.
XX		
PA		(REGC) UNIV CALIFORNIA.
XX		
PI		Meares C, Chmura A;
XX		
DR		WPI; 2001-244971/25.
DR		N-PSDB; AAF30635.
XX		
PT		Nucleic acid encoding a mutant antibody comprising a reactive site that
PT		specifically binds to a metal chelate useful as analytical agents and in
PT		clinical diagnosis, as well as in the treatment of disease, particularly
PT		cancer.
XX		
PS		Disclosure; Fig 14; 100pp; English.

XX

CC The invention provides a mutant antibody comprising a reactive site that
CC is not present in the wild-type of the antibody. The antibody also has a
CC complementarity determining region (CDR) that specifically binds to a
CC metal chelate against which the wild-type antibody is raised. The
CC reactive site of the mutant antibody is in a position proximate to or
CC within the CDR, such that the chelate and the antibody are able to form a
CC covalent bond. The present sequence is that of the light chain variable
CC region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C
CC mutation. As an example of the method of the invention, rational computer
CC -aided design was used to develop an indium-EDTA chelate to covalently
CC bind to CHA255 in vivo. The premise was to allow the chelate to bind non-
CC covalently to CHA255 bound to a tumour and then to covalently attach the
CC chelate to the antibody, thereby trapping it at the tumour site. This
CC involved cloning the variable domains of CHA255 to construct a
CC human/mouse chimeric Fab fragment that could be expressed in Escherichia
CC coli, and the synthesis and screening of benzyl-EDTA chelates carrying
CC weakly electrophilic groups capable of conjugation of the antibody in
CC vivo. This Fab can be conjugated to a targeting moiety when desired. A
CC reactive site was incorporated into the antibody by engineering a Cys
CC residue at location Asn-96 or Ser-95 of the light chain, near the region
CC of the antibody to which the chelate bound. This was accomplished by site
CC -directed mutagenesis of a nucleic acid encoding the wild-type of the
CC anti-chelate antibody

XX

SQ Sequence 218 AA;

Query Match 99.8%; Score 1132; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.9e-79;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60
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Db 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG 60

Qy 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
|
Db 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120

Qy 121 IFPPSDEQLKSGTASVVCLLNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
|
Db 121 IFPPSDEQLKSGTASVVCLLNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

Qy 181 STLTLISKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Db 181 STLTLISKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218

us-09-671-953b-7.ra1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:23:21 ; Search time 30 Seconds
(without alignments)
542.450 Million cell updates/sec

Title: US-09-671-953B-7
Perfect score: 1134
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	757	66.8	235	3	US-09-423-439-18	Sequence 18, Appl
2	750	66.1	220	3	US-08-952-235-1	Sequence 1, Appli
3	750	66.1	220	4	US-09-669-971-1	Sequence 1, Appli
4	743	65.5	233	4	US-09-472-087-15	Sequence 15, Appl
5	743	65.5	233	4	US-09-472-087-67	Sequence 67, Appl
6	739	65.2	213	3	US-08-397-411-12	Sequence 12, Appl
7	736	64.9	235	4	US-09-011-769A-27	Sequence 27, Appl
8	734	64.7	236	4	US-09-315-926A-79	Sequence 79, Appl
9	732.5	64.6	234	4	US-09-472-087-17	Sequence 17, Appl
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11	732	64.6	235	4	US-09-472-087-14	Sequence 14, Appl
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13	731.5	64.5	224	4	US-09-456-090A-84	Sequence 84, Appl
14	731.5	64.5	224	4	US-09-453-234-84	Sequence 84, Appl
15	730.5	64.4	491	4	US-10-011-125A-2	Sequence 2, Appli
16	728.5	64.2	214	3	US-08-397-411-5	Sequence 5, Appli
17	728	64.2	239	4	US-09-627-896B-22	Sequence 22, Appl

					us-09-671-953b-7.rai	
18	726.5	64.1	214	4	US-09-472-087-71	Sequence 71, Appl
19	726.5	64.1	224	4	US-09-456-090A-46	Sequence 46, Appl
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21	725	63.9	234	4	US-09-740-002-26	Sequence 26, Appl
22	724.5	63.9	234	4	US-09-740-002-24	Sequence 24, Appl
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24	724	63.8	235	3	US-09-171-945-17	Sequence 17, Appl
25	722.5	63.7	224	4	US-09-456-090A-36	Sequence 36, Appl
26	722.5	63.7	224	4	US-09-453-234-36	Sequence 36, Appl
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32	721.5	63.6	236	1	US-08-157-101A-5	Sequence 5, Appli
33	720.5	63.5	213	3	US-08-630-820-6	Sequence 6, Appli
34	720.5	63.5	213	4	US-09-273-453-6	Sequence 6, Appli
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36	719	63.4	219	3	US-09-026-985-72	Sequence 72, Appl
37	719	63.4	219	4	US-09-121-952A-72	Sequence 72, Appl
38	719	63.4	219	4	US-09-234-340A-72	Sequence 72, Appl
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ALIGNMENTS

RESULT 1

US-09-423-439-18

; Sequence 18, Application US/09423439

; Patent No. 6339070

GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles

BLAKEY, David Charles

TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L.L.P.

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423,439

FILING DATE: 09-No. 6339070-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294

FILING DATE: 05-MAY-1998

APPLICATION NUMBER: GB 9709421.3

FILING DATE: 10-MAY-1997

us-09-671-953b-7.ra

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-423-439-18

Query Match 66.8%; Score 757; DB 3; Length 235;
Best Local Similarity 71.8%; Pred. No. 7.9e-67;
Matches 155; Conservative 15; Mismatches 40; Indels 6; Gaps 3;

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Db	81	ARFSGSGSGTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEI-KRTVAAPSVFIF	139
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Qy	183	LTLSKADYEHKVKYACEVTHQGLSXPVTKSFNRGEC	218
Db	200	LTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC	235

us-09-671-953b-7.rapb

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:34:17 ; Search time 113.5 Seconds
(without alignments)
802.937 Million cell updates/sec

Title: US-09-671-953B-7
Perfect score: 1134
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1083	95.5	218	16	US-10-625-047-27	Sequence 27, Appl

us-09-671-953b-7.rapb						
2	1083	95.5	218	17	US-10-631-258-27	Sequence 27, Appl
3	1083	95.5	218	18	US-10-350-555-27	Sequence 27, Appl
4	1082	95.4	218	16	US-10-625-047-28	Sequence 28, Appl
5	1082	95.4	218	17	US-10-631-258-28	Sequence 28, Appl
6	1082	95.4	218	18	US-10-350-555-28	Sequence 28, Appl
7	759.5	67.0	235	16	US-10-723-003-42	Sequence 42, Appl
8	759.5	67.0	235	20	US-11-004-639-42	Sequence 42, Appl
9	759	66.9	213	17	US-10-822-231-3	Sequence 3, Appli
10	759	66.9	213	18	US-10-880-028-49	Sequence 49, Appl
11	759	66.9	213	18	US-10-880-320-49	Sequence 49, Appl
12	754.5	66.5	235	20	US-11-019-180-2	Sequence 2, Appli
13	753	66.4	213	14	US-10-150-475A-8	Sequence 8, Appli
14	753	66.4	213	16	US-10-704-522-8	Sequence 8, Appli
15	753	66.4	213	16	US-10-645-215-8	Sequence 8, Appli
16	753	66.4	213	20	US-11-136-538-9	Sequence 9, Appli
17	751	66.2	213	14	US-10-150-475A-4	Sequence 4, Appli
18	751	66.2	213	16	US-10-704-522-4	Sequence 4, Appli
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20	751	66.2	213	20	US-11-136-538-8	Sequence 8, Appli
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22	750	66.1	220	14	US-10-232-408-1	Sequence 1, Appli
23	746	65.8	215	17	US-10-724-274-32	Sequence 32, Appl
24	746	65.8	215	18	US-10-830-956-32	Sequence 32, Appl
25	745	65.7	213	15	US-10-435-299-12	Sequence 12, Appl
26	745	65.7	213	17	US-10-822-300-135	Sequence 135, App
27	744	65.6	215	17	US-10-818-068-26	Sequence 26, Appl
28	744	65.6	215	17	US-10-822-300-141	Sequence 141, App
29	744	65.6	215	17	US-10-724-274-26	Sequence 26, Appl
30	744	65.6	215	18	US-10-830-956-26	Sequence 26, Appl
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32	743.5	65.6	234	14	US-10-225-108A-4	Sequence 4, Appli
33	743.5	65.6	234	15	US-10-461-148-2	Sequence 2, Appli
34	743	65.5	233	14	US-10-153-382-11	Sequence 11, Appl
35	743	65.5	233	16	US-10-612-497-15	Sequence 15, Appl
36	743	65.5	233	16	US-10-612-497-67	Sequence 67, Appl
37	743	65.5	233	16	US-10-776-649-15	Sequence 15, Appl
38	743	65.5	233	16	US-10-776-649-67	Sequence 67, Appl
39	743	65.5	233	20	US-11-085-368-11	Sequence 11, Appl
40	743	65.5	233	20	US-11-085-368-47	Sequence 47, Appl
41	739.5	65.2	234	15	US-10-045-674-587	Sequence 587, App
42	739	65.2	215	15	US-10-307-724-122	Sequence 122, App
43	739	65.2	215	16	US-10-737-290-122	Sequence 122, App
44	739	65.2	239	16	US-10-737-290-142	Sequence 142, App
45	738	65.1	213	15	US-10-474-832-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
 US-10-625-047-27
 ; Sequence 27, Application US/10625047
 ; Publication No. US20040198962A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meares, Claude
 ; APPLICANT: Corneillie, Todd
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Multi-Functional Antibodies
 ; FILE REFERENCE: 023070-130910US
 ; CURRENT APPLICATION NUMBER: US/10/625,047
 ; CURRENT FILING DATE: 2003-07-22
 ; PRIOR APPLICATION NUMBER: US 10/350,555
 ; PRIOR FILING DATE: 2003-01-23

us-09-671-953b-7.rapb

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; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
;   LENGTH: 218
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:native cloned
;   OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region
;   OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody
;   OTHER INFORMATION: kappa light chain constant region (TTCL)
US-10-625-047-27
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Query Match 95.5%; Score 1083; DB 16; Length 218;
Best Local Similarity 95.9%; Pred. No. 1.2e-84;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db      1 RSAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGNNRPPG 60

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RESULT 2

US-10-631-258-27

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; Sequence 27, Application US/10631258
; Publication No. US20050026263A1
; GENERAL INFORMATION:
;   APPLICANT: Meares, Claude
;   APPLICANT: Corneillie, Todd
;   APPLICANT: The Regents of the University of California
;   TITLE OF INVENTION: Multi-Functional Antibodies
;   FILE REFERENCE: 023070-130920US
;   CURRENT APPLICATION NUMBER: US/10/631,258
;   CURRENT FILING DATE: 2003-07-31
;   PRIOR APPLICATION NUMBER: US 10/350,555
;   PRIOR FILING DATE: 2003-01-23
;   PRIOR APPLICATION NUMBER: US 10/625,047
;   PRIOR FILING DATE: 2003-07-22
;   NUMBER OF SEQ ID NOS: 72
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 27
;   LENGTH: 218
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:native cloned
;   OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region
;   OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody
;   OTHER INFORMATION: kappa light chain constant region (TTCL)
US-10-631-258-27
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us-09-671-953b-7.rapb

Query Match 95.5%; Score 1083; DB 17; Length 218;
Best Local Similarity 95.9%; Pred. No. 1.2e-84;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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RESULT 3

US-10-350-555-27

; Sequence 27, Application US/10350555

; Publication No. US20040146934A1

GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130900US

; CURRENT APPLICATION NUMBER: US/10/350,555

; CURRENT FILING DATE: 2003-01-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 27

; LENGTH: 218

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:native cloned

; OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region

; OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody

; OTHER INFORMATION: kappa light chain constant region (TTCL)

US-10-350-555-27

Query Match 95.5%; Score 1083; DB 18; Length 218;
Best Local Similarity 95.9%; Pred. No. 1.2e-84;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db     61  VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120

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RESULT 4

US-10-625-047-28

; Sequence 28, Application US/10625047

; Publication No. US20040198962A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130910US

; CURRENT APPLICATION NUMBER: US/10/625,047

; CURRENT FILING DATE: 2003-07-22

; PRIOR APPLICATION NUMBER: US 10/350,555

; PRIOR FILING DATE: 2003-01-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 28

; LENGTH: 218

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:N53C cloned

; OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable

; OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin

; OTHER INFORMATION: antibody kappa light chain constant region (TTCL)

US-10-625-047-28

Query Match 95.4%; Score 1082; DB 16; Length 218;

Best Local Similarity 95.9%; Pred. No. 1.5e-84;

Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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US-10-631-258-28

; Sequence 28, Application US/10631258

; Publication No. US20050026263A1

; GENERAL INFORMATION:

; APPLICANT: Meares, Claude

; APPLICANT: Corneillie, Todd

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: Multi-Functional Antibodies

; FILE REFERENCE: 023070-130920US

; CURRENT APPLICATION NUMBER: US/10/631,258

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                                us-09-671-953b-7.rapb
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US 10/350,555
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US 10/625,047
; PRIOR FILING DATE: 2003-07-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 218
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:N53C cloned
;   OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable
;   OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin
;   OTHER INFORMATION: antibody kappa light chain constant region (TTCL)
US-10-631-258-28

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Query Match          95.4%;  Score 1082;  DB 17;  Length 218;
Best Local Similarity 95.9%;  Pred. No. 1.5e-84;
Matches 209;  Conservative 0;  Mismatches 9;  Indels 0;  Gaps 0;

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Qy    121  IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180

Qy    181  STLTLKADYEEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
         |||||||||||||||||||
Db    181  STLTLKADYEEKHKVYACEVTHQGLSLPVTKSFNRGEC 218

```

```

RESULT 6
US-10-350-555-28
; Sequence 28, Application US/10350555
; Publication No. US20040146934A1
; GENERAL INFORMATION:
;   APPLICANT: Meares, Claude
;   APPLICANT: Corneillie, Todd
;   APPLICANT: The Regents of the University of California
;   TITLE OF INVENTION: Multi-Functional Antibodies
;   FILE REFERENCE: 023070-130900US
;   CURRENT APPLICATION NUMBER: US/10/350,555
;   CURRENT FILING DATE: 2003-01-23
;   NUMBER OF SEQ ID NOS: 72
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 218
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:N53C cloned
;   OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable
;   OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin
;   OTHER INFORMATION: antibody kappa light chain constant region (TTCL)
US-10-350-555-28

```


us-09-671-953b-7.rapb

Query Match 95.4%; Score 1082; DB 18; Length 218;
Best Local Similarity 95.9%; Pred. No. 1.5e-84;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy	1	RSAAVTQESALTTSPGETVTLTCSRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG	60
Db	1	RSAAVTQESALTTSPGETVTLTCSRSTGAVTTSNYANWVQEKPDHLFTGLIGGCNNRPPG	60
Qy	61	VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF	120
Db	61	VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWFVFGGGTKLTVLSRTVAAPSVF	120
Qy	121	IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	180
Db	121	IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS	180
Qy	181	STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC	218
Db	181	STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC	218

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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:22:51 ; Search time 25.5 Seconds
(without alignments)
822.559 Million cell updates/sec

Title: US-09-671-953B-7
Perfect score: 1134
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	739	65.2	215	2	JE0242	Ig kappa chain NIG
2	735	64.8	215	2	JE0244	Ig kappa chain NIG
3	728.5	64.2	214	2	PC4156	Ig lambda chain V
4	721	63.6	215	2	JE0243	Ig kappa chain NIG
5	678.5	59.8	216	2	JE0241	Ig kappa chain Am3
6	672	59.3	215	2	A23746	Ig kappa chain V-I
7	578.5	51.0	135	2	S52059	JC-kappa protein -
8	549.5	48.5	240	2	S06084	Ig kappa chain pre
9	547.5	48.3	287	4	PC4402	pelB leader/Ig hea
10	544	48.0	106	1	K3HU	Ig kappa chain C r
11	541	47.7	128	2	S52450	Ig lambda chain V
12	534.5	47.1	220	2	A31790	Ig kappa chain V r
13	533	47.0	129	1	L1MS4E	Ig lambda-1 chain

14	526	46.4	235	2	S25058	Ig kappa chain - m
15	525	46.3	113	2	S06819	Ig lambda chain V
16	523.5	46.2	112	2	S06818	Ig lambda chain V
17	521	45.9	106	2	S20654	Ig lambda chain V
18	513.5	45.3	114	2	S06820	Ig lambda chain V
19	511	45.1	219	2	S38865	Ig kappa chain - m
20	511	45.1	225	2	S37484	Ig kappa chain - m
21	509	44.9	99	2	A37927	Ig kappa chain C r
22	504.5	44.5	234	2	S14237	Ig kappa chain pre
23	503	44.4	99	2	S26653	Ig kappa chain C r
24	502.5	44.3	230	2	S33161	Ig kappa chain - s
25	500	44.1	113	2	B54256	Ig lambda-1 chain
26	499.5	44.0	114	2	S06822	Ig lambda chain V
27	498	43.9	129	1	L2MS35	Ig lambda-2 chain
28	497.5	43.9	214	2	S68212	Ig kappa chain (Ma
29	497.5	43.9	218	2	S68241	Ig kappa chain V r
30	495.5	43.7	225	2	JL0029	Ig kappa chain pre
31	495.5	43.7	234	2	S01320	Ig kappa chain pre
32	492.5	43.4	218	2	JC5810	monoclonal antibod
33	490	43.2	217	2	S42772	Ig kappa chain - m
34	488.5	43.1	99	2	PH1089	Ig lambda chain V
35	488	43.0	219	2	S16112	Ig kappa chain V r
36	486	42.9	99	2	S14582	Ig lambda chain V
37	486	42.9	113	2	S06821	Ig lambda chain V
38	485	42.8	235	2	S25749	Ig lambda chain -
39	484.5	42.7	219	2	PC4203	Ig kappa chain (mo
40	478	42.2	97	2	PH1090	Ig lambda chain V
41	478	42.2	116	1	L1MSV	Ig lambda-1 chain
42	478	42.2	219	2	S52028	Ig kappa chain - m
43	473	41.7	99	2	S14584	Ig lambda chain V
44	473	41.7	100	2	PH1088	Ig lambda chain V
45	469.5	41.4	210	2	A56169	Ig kappa chain V r

ALIGNMENTS

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C;Species: Homo sapiens (man)

C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C;Accession: JE0242

R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.

submitted to JIPID, November 1998

A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Multiple deletions found in a VkIV protein.

A;Reference number: JE0241

A;Accession: JE0242

A;Molecule type: protein

A;Residues: 1-215 <ALI>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 739; DB 2; Length 215;
Best Local Similarity 70.4%; Pred. No. 1.4e-48;

Matches 152; Conservative 17; Mismatches 43; Indels 4; Gaps 3;

Qy	4	VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP	62
		:: :: :: : ::: :: : ::: ::	
Db	3	VLTQSPGTLSLSPGERATLSCRAS--QSVSNYYLAWYQOKPGQAPSLLIYDASSRATGIP	60
Qy	63	ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF	122
		: : :: : : :	
Db	61	DRFSGSGSGTDFILTIISGLEPEDFAVYYCQQYDRPPWTFGQGTKVEI-KRTVAAPSVFIF	119
Qy	123	PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSS	182
Db	120	PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSS	179
Qy	183	LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC	218
Db	180	LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	215

us-09-671-953b-7.rup

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:22:03 ; Search time 116.5 Seconds
(without alignments)
958.225 Million cell updates/sec

Title: US-09-671-953B-7
Perfect score: 1134
Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries.

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	732	64.6	235	2	Q6GMW0	Q6gmw0 homo sapien
2	731	64.5	235	2	Q6PJF2	Q6pjf2 homo sapien
3	728	64.2	236	2	Q6GMW1	Q6gmw1 homo sapien
4	725	63.9	234	2	Q7Z473	Q7z473 homo sapien
5	722.5	63.7	236	2	Q7Z3Y4	Q7z3y4 homo sapien
6	721	63.6	235	2	Q6GMV9	Q6gmv9 homo sapien
7	720.5	63.5	236	2	Q6GMX9	Q6gmx9 homo sapien
8	720.5	63.5	236	2	Q6PIH7	Q6pih7 homo sapien
9	719.5	63.4	236	2	Q6P5S8	Q6p5s8 homo sapien
10	717.5	63.3	236	2	Q6PIL8	Q6pil8 homo sapien
11	714.5	63.0	236	2	Q6GMX0	Q6gmx0 homo sapien
12	709.5	62.6	236	2	Q6GMX8	Q6gmx8 homo sapien
13	706.5	62.3	236	2	Q6PIH4	Q6pih4 homo sapien
14	699	61.6	236	2	Q6PIT5	Q6pit5 homo sapien
15	695	61.3	240	2	Q6PIH6	Q6pih6 homo sapien
16	692	61.0	239	2	Q8NEK0	Q8nek0 homo sapien
17	692	61.0	239	2	Q8TCD0	Q8tcd0 homo sapien
18	663	58.5	239	2	Q6P491	Q6p491 homo sapien
19	564.5	49.8	120	2	Q6P5R5	Q6p5r5 homo sapien
20	544	48.0	106	1	KAC_HUMAN	P01834 homo sapien
21	539	47.5	129	1	LV1E_MOUSE	P01727 mus musculus

					us-09-671-953b-7.rup	
22	534	47.1	129	1	LV1D_MOUSE	P01726 mus musculu
23	533	47.0	129	1	LV1B_MOUSE	P01724 mus musculu
24	527	46.5	129	2	Q8VDE2	Q8vde2 mus musculu
25	525	46.3	110	1	LV1C_MOUSE	P01725 mus musculu
26	518.5	45.7	113	2	Q8CGS1	Q8cgs1 mus musculu
27	516.5	45.5	238	2	Q66JS7	Q66js7 mus musculu
28	512.5	45.2	109	2	Q9ET13	Q9et13 mus musculu
29	505.5	44.6	236	2	Q7TS98	Q7ts98 mus musculu
30	498	43.9	129	1	LV2B_MOUSE	P01729 mus musculu
31	498	43.9	219	2	Q65ZC0	Q65zc0 mus musculu
32	493.5	43.5	241	2	Q63ZX4	Q63zx4 mus musculu
33	478	42.2	117	1	LV1A_MOUSE	P01723 mus musculu
34	450	39.7	117	1	LV2A_MOUSE	P01728 mus musculu
35	441.5	38.9	236	2	Q8NEJ1	Q8nej1 homo sapien
36	440	38.8	235	2	Q6IN99	Q6in99 homo sapien
37	434	38.3	248	2	Q7SYU1	Q7syu1 xenopus lae
38	432.5	38.1	236	2	Q6IPQ0	Q6ipq0 homo sapien
39	430.5	38.0	236	2	Q6PIQ7	Q6piq7 homo sapien
40	430	37.9	233	2	Q8TBC9	Q8tbc9 homo sapien
41	428.5	37.8	230	2	Q7Z2U3	Q7z2u3 homo sapien
42	427.5	37.7	236	2	Q6GMV7	Q6gmv7 homo sapien
43	425.5	37.5	234	2	Q7Z2U7	Q7z2u7 homo sapien
44	424	37.4	231	2	Q6GNB8	Q6gnb8 xenopus lae
45	424	37.4	233	2	Q8N5F4	Q8n5f4 homo sapien

ALIGNMENTS

RESULT 1

Q6GMW0

ID Q6GMW0 PRELIMINARY; PRT; 235 AA.
AC Q6GMW0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

us-09-671-953b-7.rup

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC073792; AAH73792.1; -.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; C1-set; 1.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGc1; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 64.6%; Score 732; DB 2; Length 235;
 Best Local Similarity 70.3%; Pred. No. 5e-56;
 Matches 154; Conservative 16; Mismatches 39; Indels 10; Gaps 5;

Qy	4	VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP	62
		: : :	
Db	23	VMTQSPATLSVSPGERATLSCRAS---QSISSNNLAWYQQRPGQAPRLLIYGASSRVTGIP	79
Qy	63	ARFSGSLIGDKAALTITGAQTEDEARYFCAL---WYCNLWVFGGGTKLTVLSRTVAAPSV	119
		: :	
Db	80	GRFSGSGSGTEFTLSISLQSEDAVYFCQYNDWL--LYTFGQGTKLEI-KRTVAAPSV	136
Qy	120	FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL	179
Db	137	FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL	196
Qy	180	SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC	218
Db	197	SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	235